CLAIMS

What is claimed is:

1. A method for obtaining a probe that hybridizes to a gene in a PKS gene cluster comprising:

a) identifying amplimers produced at higher frequency from amplification of cDNA from RNA of a producer cell and degenerate PCR primers that hybridize to consensus regions of gene sequences encoding a PKS domain, compared to amplification of genomic DNA of the producer cell using the same primers; and,

b) using the sequences of the amplimers selected in (a) for designing one or more probes for cloning genes in a PKS gene cluster.

2. The method of claim 1 wherein the PKS domain is selected from the group consisting of KR, AT, ACP, KR, DH, ER, and TE.

3. The method of claim 2 wherein the PKS domain is KS.

4. The method of claim 1 wherein the cDNA is prepared from RNA collected at least two different times.

5. The method of claim 1 wherein the cDNA is prepared from RNA collected from cells cultured under at least two different production conditions.

6. The method of claim 1 wherein the cDNA is prepared from RNA from cells collected prior to the time of maximum polyketide production.

7. The method of claim 1 wherein at least one probe has the sequence the same length as and identical or exactly complementary to an amplimer.

8. The method of claim 1, further comprising using the probes in screen a genomic DNA library of the producer cell for clones encoding sequence of a gene in a PKS gene cluster.

9. A method for detecting a nucleic acid encoding a PKS gene comprising hybridizing a probe obtained by the method of claim 1 to said nucleic acid and detecting the hybridization complex.

10. A method for obtaining a probe that hybridizes to a gene encoding a first PKS gene comprising:

a) determining the sequences of a plurality of amplimers prepared using degenerate PCR primers that hybridize to consensus regions of gene sequences encoding a PKS domain;

b) determining phylogenetic similarity for the amplimers in (a) and plurality of sequences encoding a domains of a gene or genes encoding one or more PKS related to said first PKS;

c) selecting the amplimer sequences from (a) that are most closely related to one or more domain-encoding sequences in (b); and,

d) using the sequences selected in (c) for designing probes that hybridize to said first PKS gene.

11. The method of claim 10 wherein the domain is selected from the group consisting of KR, AT, ACP, KR, DH, ER, and TE.

12. The method of claim 11 wherein the domain is KS.

13. The method of claim 10 wherein determining phylogenetic similarity tree is done using a computer running ClustalW software.

14. The method of claim 10 wherein the sequence of the first PKS gene is not known.

15. A method for detecting a nucleic acid encoding a PKS gene comprising hybridizing a probe obtained by the method of claim 11 to said nucleic acid and detecting the hybridization complex.